

SEQUENCE LISTING

<110> Sauter, Margret M.
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTION UNDER HYPOXIC
CONDITIONS

<130> CropDesign

<140>

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<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 872

<212> DNA

<213> Rice

<220>

<221> CDS

<222> (69)..(668)

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1 5 10

gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
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cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
35 40 45

gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
50 55 60

ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
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gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
80 85 90

00785730-021501

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 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446
 Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
 115 120 125
 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494
 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
 130 135 140
 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga 542
 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
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 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
 160 165 170
 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa 638
 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
 175 180 185 190
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 <213> Rice

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 35 40 45
 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
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gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
1 5 10
gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
15 20 25
cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
30 35 40
gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
45 50 55
gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
60 65 70 75
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<213>	Rice

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Lys	Ile	Arg	Glu	Ala	Arg	Gly	Tyr	Ser	Tyr	Met	Asp	Ile	Cys	Asp	Val
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Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125

ggg gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

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Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175

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Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
Asn Ala Ala Ala
195

aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691

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Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

09785739-021601

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Ile	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu	Pro	Ala	Arg	Gln
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Glu	Tyr	Val	Glu	Thr	Phe	Val	Asn	Ala	Asp	Gly	Ala	Gly	Arg	Ala	Val
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				20					25					30		
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Glu	Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	
			35					40					45			
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Tyr	Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn	
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Tyr	Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp	
	80				85					90					95	
gag	gag	ata	cgt	tac	tgt	ctg	gaa	ggg	agt	gga	tat	ttt	gat	gtg	aga	335
Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	
				100					105					110		
gac	aag	gat	gat	cgc	tgg	att	cgc	atc	tgg	atg	aag	gcc	ggg	gat	atg	383
Asp	Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met	
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Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	
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 Pro Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile
 160 165 170 175

aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa 572
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 35 40 45
 Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly Tyr
 50 55 60
 Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn Tyr
 65 70 75 80
 Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp Glu
 85 90 95
 Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp
 100 105 110
 Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met Ile
 115 120 125
 Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp Asn
 130 135 140
 Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro
 145 150 155 160
 Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile Lys
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 Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
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0075730-021604

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<211> 889
<212> DNA
<213> Soybean

<220>
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<222> (32)..(634)

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Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
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gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg 148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu
25 30 35

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
40 45 50 55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat 292
Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
75 80 85

tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat 340
Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp
90 95 100

gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc 484
Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser
140 145 150

aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act 532
Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
155 160 165

cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc 580
Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
170 175 180

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628
Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
185 190 195

gcg taa gatctgggtc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684
Ala
200

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ttggttatgcc ttgatgtacc ctgccagtg tttttgttgc ctgtccctgt ataaagattg 804

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<213> Soybean

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35 40 45
Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala
50 55 60
Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg
65 70 75 80
Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro
85 90 95
Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr
100 105 110
Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val
115 120 125
Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly
130 135 140
Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
145 150 155 160
Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp
165 170 175
Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
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Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
195 200 205
Thr Ala
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 <213> Cotton

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Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
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gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149
Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
                                   25                               30                               35

gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197
Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
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aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245
Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
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tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293
Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
                                   75                               80                               85

tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341
Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
                                   90                               95                               100

gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389
Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
105                               110                               115

gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437
Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120                               125                               130                               135

ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
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Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
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Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
170 175 180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
185 190 195

gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745

aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805

ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtatctt ctacatttta 865

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<212> PRT

<213> Cotton

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35 40 45
Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
50 55 60
Lys Ile Arg Glu Glu Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe
85 90 95
Glu Glu His Ile His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp His Asn Asp Lys Trp Ile Arg Val
115 120 125
Trp Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His
130 135 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Asp Pro Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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<221> CDS  
<222> (1)..(564)
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Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
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gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag 144
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
35 40 45

ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga 192
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
50 55 60

aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat 240
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65 70 75 80

aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat 288
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
85 90 95

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		100						105					110			

ttc	gat	gtg	agg	gac	aag	gag	gac	cag	tgg	atc	cgg	atc	ttc	atg	gag	384
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu	
		115					120					125				

aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg 432
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
130 135 140

gtg	gac	gag	aag	aac	tac	acg	aag	gcc	atg	cgg	ctg	ttt	gtg	gga	gaa	480
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu	
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          165                      170                      175

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ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtgcc 574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

tgggaactaa cacgtgcctc gtaaagggtcc ccaatgtaat gaactgagca gaaaattcaa 634
tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694
ttatttgatc agaatatattt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754
gtcaccttca ttttctgtaa ctcaatcaag actgggtgggt ccatggccct gtgttagttc 814
attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
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<211> 187

<212> PRT

<213> Human

<400> 14

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Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala
			20					25					30		
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys
		35					40					45			
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg
	50					55					60				
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp
	65				70					75				80	
Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Met	Phe	Tyr	Glu	Glu	His
			85						90				95		
Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ser	Gly	Tyr
			100					105					110		
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu
		115					120					125			
Lys	Gly	Asp	Met	Val	Thr	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr
		130				135					140				
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu
	145				150					155					160
Pro	Val	Trp	Thr	Ala	Tyr	Asn	Arg	Pro	Ala	Asp	His	Phe	Glu	Ala	Arg
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Gly	Gln	Tyr	Val	Lys	Phe	Leu	Ala	Gln	Thr	Ala					
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 <212> DNA
 <213> Mouse

<220>
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 <222> (17)..(556)

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 Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
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gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148
 Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
 30 35 40

gag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196
 Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
 45 50 55 60

tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244
 Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
 65 70 75

tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat 292
 Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
 80 85 90

gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg 340
 Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
 95 100 105

gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg 388
 Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
 110 115 120

att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag 436
 Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
 125 130 135 140

aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca 484
 Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
 145 150 155

cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg 532
 Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
 160 165 170

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agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt 586
Ser Phe Leu Glu Gly Thr Ala
      175                      180

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gtgaatctcc	tgctgtggta	accgaatgga	aagttgctca	cttttctgct	tttgtatttg	646
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agcctctcta	aaagtgaagt	ttacatggaa	gccacaaaaa	tgtgaaaaag	tgaccttaat	766
tttccctaac	tgtcaagact	tagagggtata	ggagccctgg	attggtatgt	gcattcatgc	826
atggccaatc	ttcatctccc	agatcttttag	gtgtctgttg	gtgtgaagct	atgcctcctg	886
caagagggca	gttataacca	gcacaactaa	ccagatgacg	tttttctcct	ttgctgattg	946
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 <222> (36)..(581)

<400> 17

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Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys
                                   10                               20

ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga      149
Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
                                   25                               35

gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa      197
Val Phe His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
                                   40                               50

ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata      245
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
55                               60                               65                               70

acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg      293
Thr Ile His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
                                   75                               80                               85

ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg      341
Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
                                   90                               95                               100

gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc      389
Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
                                   105                               110                               115

cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att      437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
                                   120                               125                               130

tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt      485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
135                               140                               145                               150

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat      533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
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gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581
 Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 170 175 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcgggtgcct tanacagaca 641
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 attat 706

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 20 25 30
 Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
 35 40 45
 Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
 50 55 60
 Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
 65 70 75 80
 Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
 85 90 95
 Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
 100 105 110
 Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
 115 120 125
 Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
 130 135 140
 Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
 145 150 155 160
 Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
 165 170 175
 Ser Leu Gly Ser Ser
 180